REMARKS

Reconsideration and withdrawal of the rejections of the claims, in view of the amendments and remarks herein, is respectfully requested. Claim 1 is amended, claims 32-43 are canceled, and claims 50-55 are added. The amendments are intended to advance the application and are not intended to concede to the correctness of the Examiner's position or to prejudice the prosecution of the claims prior to amendment, which claims are in a continuation of the present application. Claims 1-31 and 44-55 are pending.

Claims 32-43 are canceled solely in response to the Restriction Requirement and without prejudice to their presentation in an appropriately-filed continuing application.

Support for the amendments to claim 1, and new claims 50-55, is found, for instance, in originally-filed claims 1, 32 and 34, and page 6, lines 21-29, page 10, lines 10-11, page 11, lines 3-9, page 13, lines 16-25, page 19, lines 24-28, and page 20, lines 3-5 and 19-23. No new subject matter has been added.

The 35 U.S.C. § 112, First Paragraph, Rejections

Claims 1, 8-9, 15-19, 23, 25, and 43-49 were rejected under 35 U.S.C. § 112, first paragraph, as lacking adequate description. Specifically, the Examiner asserts that the specification teaches only a single representative species of SEQ ID Nos. 2-4 and fails to describe any other representative species by any identifying characteristics or properties other than being capable of hybridizing to SEQ ID NO:2, 3 or 4. The Examiner also asserts that one skilled in the art cannot envision the detailed structure of sequences having, for example, at least 80% identity to SEQ ID NO:2, 3 or 4. This rejection, as it may be maintained with respect to the pending claims, is respectfully traversed.

The Examiner is respectfully reminded that Applicant need not teach what is well know to the art. *vanA* sequences, including *vanA*-specific probes and primers, were well known to the art, as were amplification and hybridization assays to detect those sequences (see Petrich et al., Mol. Cell Probes, 13:275 (1999)) and U.S. Patent No. 6,274,316; both of record). Moreover, Applicant's specification clearly identifies the nucleotide sequence corresponding to nucleotides 870 to 896, 851 to 868 and 898 to 917 of *vanA* (see Figure 1 and SEQ ID NOs. 2-4).

Further, the probe recited in claim 1 hybridizes to *van*A nucleic acid in a sample and to particular *vanA* sequences, i.e., hybridizes to SEQ ID NO:3 or its complement, is of a particular length and has sequences with a certain percent identity to SEQ ID NO:3 or its complement. Accordingly, the recited *vanA*-specific probes have a common structure and function.

Similarly, the primers recited in claim 1 hybridize to particular *vanA* sequences, i.e., hybridize to the complement of SEQ ID NO:2 or SEQ ID NO:4, are of a particular length, have sequences with a certain percent identity to the complement of SEQ ID NO:2 or SEQ ID NO:4, and amplify *van*A nucleic acid. Thus, the recited primers have a common structure and function.

Moreover, one of skill in the art can clearly envision variants of any of SEQ ID Nos. 2-4 with a specific percent sequence identity thereto. For example, SEQ ID NO:3 corresponds to CCGGTGGCAGCTACGTTT (18 nucleotides). 80% of 18 is 14.4. Therefore, probes within the scope of invention include those with up to 3 nucleotide substitutions in SEQ ID NO:3. The following represents a set of variants of SEQ ID NO:3 with a single substitution (indicated by underlining): CGGGTGGCAGCTACGTTT, CAGGTGGCAGCTACGTTT, and CTGGTGGCAGCTACGTTT. The following represents a set of variants of SEQ ID NO:3 with two substitutions (indicated by underlining): CGGGTGGCAGCTAGGTTT, CAGGTGGCAG CTAAGTTT, and CTGGTGGCAGCTATGTTT, and the following represents a set of variants of SEQ ID NO:3 with three substitutions (indicated by underlining): CGGGGGGCAG CTAGGTTT, CAGGAGGCAGCTAAGTTT, and CTGGCGGCAGCTATGTTT.

Therefore, the specification and claims meet the "written description" requirement of 35 U.S.C. § 112(1).

Claims 1, 8-9, 15-19, 23, 25, and 43-49 were rejected under 35 U.S.C. § 112, first paragraph, as lacking adequate description (a "new matter" rejection). Specifically, the Examiner asserts that the specification does not provide support for the recited probes and primers. This rejection is respectfully traversed.

The fundamental inquiry is whether the material added by amendment was inherently contained in the original application. *Litton Sys., Inc. v. Whirlpool Corp.*, 728 F.2d 1423, 1438, 221 U.S.P.Q. 97, 106 (Fed. Cir. 1984). The issue is not whether a specific new word of a claim was used in the specification as filed but whether the concept expressed by the word was present. *In re Anderson*, 471 F.2d 1237, 176 U.S.P.Q. 331 (C.C.P.A. 1973).

As filed, claim 1 recited that the *vanA*-specific oligonucleotide probe comprises sequences which include sequences substantially corresponding to nucleotides 870 to 896 of the *vanA* gene, the complement thereof, or a portion thereof, sequences substantially corresponding to nucleotides 851 to 868 of the *vanA* gene, the complement thereof, or a portion thereof, or sequences substantially corresponding to nucleotides 898 to 917 of the *vanA* gene, the complement thereof, or a portion thereof.

Claim 32 (as filed) is directed to an oligonucleotide composition comprising a first oligonucleotide comprising sequences substantially corresponding to nucleotides 870 to 896 of the *vanA* gene, the complement thereof, or a portion thereof, an oligonucleotide comprising sequences substantially corresponding to nucleotides 851 to 868 of the *vanA* gene the complement thereof, or a portion thereof, an oligonucleotide comprising sequences substantially corresponding to nucleotides 898 to 917 of the *vanA* gene, the complement thereof, or a portion thereof, or a combination thereof, wherein the oligonucleotide hybridizes under stringent hybridization conditions to *vanA* DNA. Claim 34 (as filed) depends on claim 32, and is directed to at least one oligonucleotide that has the length and sequence of any of SEQ ID NOs:2-4.

Pages 10 and 11 of the specification disclose that:

An "oligonucleotide" is a polynucleotide having two or more nucleotide subunits covalently joined together.

A "primer" is a single-stranded polyoligonucleotide that combines with a complementary single-stranded target to form a double-stranded hybrid, which primer in the presence of a polymerase and appropriate reagents and conditions, results in nucleic acid synthesis.

A "probe" is a single-stranded polynucleotide that combines with a complementary single-stranded target polynucleotide to form a double-stranded hybrid.

Page 6 of the specification discloses:

In one embodiment, the oligonucleotides of the invention include sequences substantially corresponding to nucleotides 851 to 868 of the *vanA* gene (SEQ ID NO:2; an exemplary *vanA* gene has SEQ ID NO:1 from *E. faecium* pIP816 gi 43335, also see Figure 1, Accession No. X56895 which corresponds to SEQ ID NO:11), or the complement thereof, or a portion thereof; sequences substantially corresponding to nucleotides 870 to 896 of the *vanA* gene (SEQ ID NO:3), the complement thereof, or a portion thereof; sequences substantially corresponding to nucleotides 898 to 917 of the *vanA* gene (SEQ ID NO:4), the complement thereof, or a portion thereof...

The Example discloses the use of primers having SEQ ID Nos. 2 and 4 to amplify *van*A-specific sequences in a biological sample and a probe having SEQ ID NO:3 to detect *van*A-specific sequences in a sample.

In the Amendment filed on May 30, 2007, Applicant indicated that support for the amendments to claim 1 is found, for instance, at page 13, lines 19-25, page 19, lines 24-28, and page 20, lines 3-5 and 20-22 of the specification. Page 13 discloses that:

> One skilled in the art will understand that probes or primers that substantially correspond to a reference sequence or region can vary from that reference sequence or region and still hybridize to the same target nucleic acid sequence. Probes of the present invention substantially correspond to a nucleic acid sequence or region if the percentage of identical bases or the percentage of perfectly complementary bases between the probe and its target sequence is from 100% to 80% or from 0 base mismatches in a 10 nucleotide target sequence to 2 bases mismatched in a 10 nucleotide target sequence. In one embodiment, the percentage is from 100% to 85%. In another embodiment this percentage is from 90% to 100%; and in yet other embodiments, this percentage is from 95% to 100%.

Page 19 discloses that:

> Preferred methods for detecting the presence of the *vanA* or *vanB* gene, include the step of contacting a test sample with at least two oligonucleotide primers under conditions that preferentially amplify *vanA* and/or *vanB* sequences....While oligonucleotides probes of different lengths and base composition may be used for detecting the *vanA* gene or the *vanB* gene, preferred oligonucleotides have lengths from 15 up to 40 nucleotides and are sufficiently homologous to the target nucleic acid to permit amplification of a *vanA* or *vanB* template and/or hybridization to such a template under high stringency conditions.

Page 20 discloses that:

> Preferred primers and probes have sequences of up to 40 nucleotides in length and preferably have at least 17 contiguous nucleotides corresponding to sequences in the *vanA* gene or the *vanB* gene, or the complement thereof... Preferably, the probes specifically hybridize to *vanA* or *vanB* DNA only under conditions of high stringency. Under these conditions only highly complementary nucleic acid hybrids will form (i.e., those having at least 14 out of 17 bases in a contiguous series of bases being complementary). Hybrids will not form in the absence of a sufficient degree of complementarity.

Thus, the specification clearly provides support for the recited probes and primers.

Therefore, withdrawal of the 35 U.S.C. § 112(1) "written description" rejections is respectfully requested.

The 35 U.S.C. § 112, Second Paragraph, Rejections

Claims 1, 8-9, 15-19, 23, 25, and 43-49 were rejected under 35 U.S.C. § 112, second paragraph, as being indefinite. In particular, the Examiner asserts that the metes and bounds of the probes and primers is unclear and "capable of hybridizing" is indefinite. This rejection, as it may be maintained with respect to the pending claims, is respectfully traversed.

It is Applicant's position that the metes and bounds of the recited primers and probe are clear. That is, the probe is a *vanA*-specific oligonucleotide that forms a hybrid with *vanA* nucleic acid in a sample. The probe has 15 to 40 nucleotides with at least 80% nucleic acid sequence identity to SEQ ID NO:3 or the complement of SEQ ID NO:3, and hybridizes to SEQ ID NO:3 or its complement. Thus, the probe is of a particular length and has sequence homology to SEQ ID NO:3 or its complement.

The primers are oligonucleotides that amplify *vanA* nucleic acid. The primers have 15 to 40 nucleotides, where one primer has at least 80% nucleic acid sequence identity to SEQ ID NO:2, and the other primer has at least 80% nucleic acid sequence identity to SEQ ID NO:4. One of the primers hybridizes to the complement of SEQ ID NO:2, and the other hybridizes to the complement of SEQ ID NO:4. Hence, the primers are of a particular length and have sequence homology to SEQ ID NO:2 or SEQ ID NO:4.

Therefore, the metes and bound of the recited probe and primers is clear.

It is Applicant's position that one of skill in the art would understand the metes and bounds of the phrase "capable of hybridizing". See, e.g., Petrich et al. (Mol. Cell Probes, 13:275 (1999)) and Modrusan (U.S. Patent No. 6,274,316) (both of record) which disclose primers or probes capable of hybridizing to *van*A sequences in a biological sample. Moreover, one of skill in the art is aware that more than one set of conditions can result in the specific hybridization of two nucleic acid sequences.

Even if, assuming for the sake of argument, the metes and bounds of the phrase "capable of hybridizing" were not readily recognizable to one skilled in the art, the specification discloses particular conditions at page 20 (for amplification reactions with primers) and pages 24-25 (for

probes). Thus, the scope of the claims would be clear to a person of skilled in the art, particularly when read in light of the specification. Nevertheless, to advance the application, the language "capable of" has been deleted from the claims.

The Examiner also asserts that the term "selective" is a term of degree and based on parameters that are not in the specification or claims (page 13 of the Office Action), and points specific conditions at pages 21-22 of the specification. However, the claims do not recite "selective". Claim 1 is directed to a method which employs a probe and a sample in which amplification of *van*A nucleic acid, e.g., via PCR, may have occurred, e.g., using the recited primers. It is Applicant's position that the selection of amplification and/or hybridization conditions specific for *van*A sequences is conventional in the art, see, for instance, Petrich et al., *supra,* Patel et al., "Multiplex PCR Detection of *vanA*, *vanB*, *vanC*-1, and *vanC-2*/3 Genes in Enterococci", J. Clin. Microbiology, 35: 703 (1997); Petrich et al., "Effect of Routine Use of a Multiplex PCR for Detection of *vanA*- and *vanB*- Mediated Enterococcal Resistrance on Accuracy, Costs and Earlier Reporting", Diagnostic Microbiology and Infectious Disease, 41:215 (2001); and Satake et al., "Detection of Vancomycin-Resistant Enterococci in Fecal Samples by PCR", J. Clin. Microbiology, 35:2325 (1997); all of record.

Accordingly, withdrawal of the 35 U.S.C. § 112(2) rejection is respectfully requested.

CONCLUSION

Applicant respectfully submits that the claims are in condition for allowance and notification to that effect is earnestly requested. The Examiner is invited to telephone Applicant's attorney (612) 373-6959 to facilitate prosecution of this application.

If necessary, please charge any additional fees or credit overpayment to Deposit Account No. 19-0743.

Respectfully submitted,

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CERTIFICATE UNDER 37 CFR 1.8: The undersigned hereby certifies that this correspondence is being filed using the USPTO's electronic filing system EFS-Web, and is addressed to: Commissioner of Patents, P.O. Box 1450, Alexandria, VA 22313-1450 on this 31 day of October 2007.

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